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Evidence of carriage of minimal form of resistance island in clinical isolates of multidrug-resistant Acinetobacter baumannii

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Background: Recent studies have recognized ATPase-encoding *comM* gene as a hot spot for integration of *Acinetobacter baumannii* resistance islands. Despite the circulating of high number of multidrug-resistant *A. baumannii* (MDR-AB) isolates in Middle East countries, no information is available about the carriage of resistance island.

Methods & Materials: The clonal type of 401 nonreplicate AB isolates was determined and the interruptions in *comM* gene as well as transposition were assessed.

Results: The most of MDR-AB isolates (384 of 388; 98%) and more than half of susceptible AB isolates (9 of 13; 69%) had interrupted *comM* gene carrying integrative element. All but 6 of global clone I (GC I) isolates (196, 97%) and 2 of GC II isolates (138, 98%) contained interrupted *comM* gene.

Conclusion: This study showed the carriage of interrupted *comM* in large series of isolates, indicating the presence of minimal form of resistance island.

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Antibiotic susceptibility patterns of prevalent anaerobic gram negative bacilli in Lagos, Nigeria: A 20 year survey

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Background: The clinical significance of anaerobic bacteria is growing with advances in diagnostic technologies. Moreover, new treatment regimens are being introduced for the treatment of infections for which anaerobes are involved. It was therefore important to evaluate the impact of the changing patterns on antibiotic resistance in the Gram negative anaerobic bacteria. This report represents our experience with anaerobic infections in Nigeria from 1992–2011.

Methods & Materials: Data on prevalence and antibiotics susceptibility patterns of anaerobic bacteria in four specialist hospitals in Lagos, Nigeria from seven clinical conditions for which anaerobes were frequently isolated were analyzed. These include peritonitis following lower abdominal surgery (PLAS, 75 cases), periodontal abscess (PAB, 60), pelvic inflammatory disease (PID, 22), chronic suppurative otitis media (CSOM, 21), septic abortion (SAB, 16), dentoalveolar abscess (DAAB, 12), and bloodstream infections (BSI, 10). Data were analyzed in sub-sets of five years intervals; 1992–1996 (PA), 1997–2001 (PB), 2002–2006 (PC), and 2007–2011 (PD).

Results: The occurrences and distribution of the Gram negative bacilli (GNB) were Bacteroides, 251 (PA 45, PB 56, PC 67, PD 83), Fusobacterium, 151 (PA 34, PB 46, PC 56, PD 15), Porphyromonas, 30 (PA 3, PB 9, PC 17, PD 1), Prevotella, 127 (PA 36, PB 49, PC 34, PD 8). Fusobacterium and Porphyromonas were the most sensitive to antibiotics with no evident shift in pattern from 1992 to 2011 but showed highest sensitivity to the cephalosporins and metronidazole. Against Bacteroides and Prevotella, amoxicillin activity was least with no change in pattern over the study period. Slight but progressive resistance to the cephalosporins by Bacteroides and Prevotella occurred (22.7% for B. fragilis to ceftazidime in 1992–1996 to 28.6% in 2007–2011). Metronidazole was the most effective antibiotics with resistance not higher than 22.7% at any time by the most resistant species. The activities of the macrolides increased appreciably from 1992 to 2011 while amoxicillin-clavulanic acid activity was relatively constant.

Conclusion: These observations indicate that the changing pattern of antibiotic usage has not appreciably altered the antibiotic profile of anaerobic GNB in Nigeria.

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Transcriptional response of arnA and pmrB in relation to polymyxin resistance in Pseudomonas aeruginosa associated with surgical wound infection: A study from North-East India

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Background: **Introduction:** Polymyxins were considered as the most effective drug against infections caused by multidrug resistant *Pseudomonas aeruginosa*. The increasing resistance mechanism by these organisms has led to the development of resistance towards this group of antibiotics. This study was designed to determine the prevalence of polymyxin resistant *P. aeruginosa* from North- East

India and to detect the role of *pmr*B and *arn*A genes in resistant phenotype.

Methods & Materials: **Methods and Materials:** Consecutive non-duplicate clinical isolates of *Pseudomonas aeruginosa* were collected from the patients admitted to surgical ward of Silchar Medical College and Hospital in the duration of September 2013 to August 2014. The isolates were screened for polymyxin resistance by Kirby-Bauer disc diffusion method and the minimum inhibitory concentrations. mRNA and cDNA of five selected polymyxin resistant strains representing different MIC range were isolated in normal condition of the strain as well as after treating with $FeCl_3$ alone and $FeCl_3$ and polymyxin antibiotic. Transcriptional expression was observed for *pmr*B and *arn*A by quantitative real time PCR in reference to *P. aeruginosa* PAO1. Susceptibility pattern of these polymyxin resistant strains was performed by Kirby- Bauer disc diffusion method. DNA fingerprinting of the isolates was carried out by performing REP PCR.

Results: **Results:** A down regulated expression of *pmr*B and *arn*A was observed in polymyxin resistant strains of *P.aeruginosa* which is unique comparing to other studies. Low susceptibility rate to amikacin and gentamicin, β-lactam-β-lactamase inhibitor piperacillin-tazobactam and quinolone group of drug ciprofloxacin was shown by polymyxin resistant *P.aeruginosa* strains whereas total resistance was observed in case of third generation cephalosporin cefepime. REP PCR results showed these polymyxin resistant organisms are heterogenous by showing different clonal pattern.

Conclusion: **Conclusion:** This study highlights the urgency of obtaining knowledge on the pharmacology of polymyxins to optimize their clinical use and minimize potential for development of resistance. This will help in management of treatment and infection control due to multidrug resistant *P. aeruginosa.*

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Molecular epidemiology and spread dynamics of multi-drug resistant in A. baumannii isolated from patients and hospital environment in Bangladesh

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Background: Multidrug-resistant (MDR) *A. baumannii* has been a serious challenge in the hospitals globally including Bangladesh. The study was performed to investigate molecular epidemiology & spread dynamics of antibiotic resistant *A. baumannii* both from patients and hospital environment in Bangladesh.

Methods & Materials: A set of 49 clinical *Acinetobacter* strains were collected from five clinical microbiology labs located in Dhaka, Bangladesh during 2014-2015. Additionally, 100 samples were collected from different hospital surfaces of Dhaka Medical College Hospital. All strains and samples were cultured on CHROMagar™ Acinetobacter selective media. *A. baumannii* was identified at species level by biochemical tests&bla_{OXA-51} PCR. Resistance to 13 antibiotics under different 8 classes was determined according to EUCAST and CLSI. PCR was used to detect different resistance genes; quinolones (*qnrS1, aac6, qepA, qnrC1, qnrB1, qnrA1*), 16S methylase (*rmtA,rmtB, rmtC, rmtD, armA*)and OXAs(-*23,-24,-58,-143*). Real-time multiplex PCR were conducted for the presence of carbapenem resistant genes (*NDM, VIM, IMP, KPC* and *oxa-48*). Epidemiological typing & clonal profile was performed by rep-PCR.

Results: 95% (47/49) human and 31% (10/32) environmental isolates of *A. baumannii* had growth on CHROMagar™ agar. All clinical and 10 environmental strains carried bla_{OXA-51} gene which confirmed as *A. baumannii.* Resistance to 4 or more antibiotic classes was found in 48 clinical and 10 environmental strains. Forty clinical and all environmental strains carried bla_{OXA-23} however; bla_{OXA-58} was in one clinical strain. The predominant ciprofloxacin resistant gene was *aac6*in both clinical and environmental isolates followed by *qnrB1*in clinical isolates and *qnrC1*in environmental isolate. Only *armA* gene was found in clinical and environmental strains. None of the clinical and environmental strains were positive for other carbapenem resistant genes (*NDM, VIM, IMP, KPC*, *OXA-48*). In total, 36 different clones were identified from both patients and environment; 6 different clinical clones (AC, BC, DC, FC, HC, PC) were common in different hospitals among patients. Some of the clones (CC, RC, P3, P6) were common both in patients and environmental strains.

Conclusion: The magnitude of resistance including their phenotypes and genotypes, and clonal relatedness among clinical and environmental *A. baumannii* indicates multi-drug resistant strains were wide spread in Bangladeshi hospitals.

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Genotyping of mycobacterium tuberculosis strains isolated from patients with pulmonary drug resistant tuberculosis in Ukraine

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Background: The epidemiological situation of tuberculosis in Ukraine is extremely unfavorable – about 40 thousand people become sick on tuberculosis each year and about 10 thousand patients die. Changing of the contemporary socio-economic and environmental conditions plays an important role in the deterioration of the tuberculosis epidemic situation. Moreover drug resistance of *M.tuberculosis* is one of the main factors limiting the effectiveness of TB treatment. Due to the development of molecular genetics it has become possible to conduct genetic typing of